



RESULT 2

Db 419 YKGWVWLKLKGIVHENVVULDFSSMPSIMKINVGDPITVDPSPSECPRYGGVYAPVG 478  
 Qy 477 HRPRCPGPFKPTVTLERLKRKVRAEMKKYPPDSPEYRPLDERROKALKVLANASYGM 536  
 Db 479 HRFRRSPPFKFTVTLNLKURQVKERKMKFPPDSPEYRPLDERROKALKVLANASYGM 538

Qy 537 GWGGAWCRCACAVTAWGRHLRTAINIKLGKLVYGDPSFLTYDPKVENTK 596  
 Db 539 GWSHARWYCKCRCAAVTAWGRHLRTAINIKLGKLVYGDPSFLTYDPKVENTK 598

Qy 597 LIKEBLGEIKLKSCKVYKRLPTEAKRGRAGLLEGRIDIVGFEEVRGDWCELAKEVQKA 656  
 Db 599 FVEEGLGEIKIJKIKYKRVFFTEAKRGRAGLLEGRIDIVGFEEVRGDWCELAKEVQKA 658

Qy 657 VETVLTKESEVNKADEVYRKVVKELBEKGKPVIEKVIKVIKTSLKRUVEYTYEAAPHVAARM 716  
 Db 659 AEIVLNTGVNDKAIISYIREVKIQLRKGKVPITKLUWKLSKRIEYEDHAPMAARM 718

Qy 717 LSGCYRVSPGDKGKQVYVKGGRSQRAMPYFMKPSOIDTYDQDIIPALRLIGY 776  
 Db 719 KEAGYEVSPGDKQVYVKGGRSQRAMPYFMKPSOIDTYDQDIIPALRLIGY 777

Qy 777 FGTEKKUKASACQKTLDFLACK 801  
 Db 778 FGVTEKOLKAATVORSLFDFEAK 802

RESULT 2

Db 872515 PROBABLE DNA-DIRECTED DNA POLYMERASE APB2098 - Aeropyrum pernix (strain K1) C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #Sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000 C;Accession: E72515 R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahashi, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K.DNA.Res. 6, 83-101, 1999 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix C;Reference number: A72450; NUID:99310339; PMID:10382966 A;Accession: E72515 A;Species: preliminary A;Molecule type: DNA A;Residues: 1-784 <RAW> A;Cross-references: DDBJ:AP0000063; NID:95105654; PIDN:BAA81109.1; PID:95105797 C;Experimental source: strain K1 C;Genetics: C;Gene: APB2098 C;Superfamily: herpesvirus DNA-directed DNA polymerase

Query Match 58.1%; Score 2434; DB 2; Length 784; Best Local Similarity 59.1%; Pred. No. 3.7e-140; Matches 469; Conservative 113; Mismatches 189; Indels 22; Gaps 5;

Qy 17 GKBRQVITGIAENGERVVLDRPRPYFALLPGADPKQVQAIRALSRPKSPIGE 76  
 Db 3 GSTPVILNGRAGDQSRRVWVYGPSPRPYVLPDGSVGLDAMIRRLSPRSSPILSVE 62

Qy 77 DDKPKYFGPRRVIRTVLPEAREYRELYVNDGVEDVLEADIRPAMYLIDHDLLPP 136  
 Db 63 RVRRFFIGEVRAVKUTTVIPASTREYRVARGVVRLLEADIPPAFPIDNLYPM 122

Qy 137 TWKVKVPEAEPLENKQAFPRDKVYL-----KSRPBPYGEALAPTKLDRILARDI 187  
 Db 123 RWVYTAEVRAVVAVPHGSPVDRATSGDIRDETRIQEDFLKG-----LRVMAFDI 172

Qy 188 EVYSKGSRPRPERPVIVIAVKTDDGDEYTLFIANGKDDKPKTIREPVEVYKVPDITGY 247  
 Db 173 EVSKMRTDPKKDPUVIMIQLQKAGEJETLEADRSRDKVIAQFVERVKSIDBDVGY 232

Qy 248 NNHMFDPWMLLARRARLIGKLDVTRVGRGAEPITVHGTVSPGGLANDLVDYKAEEMPEK 307  
 Db 249 NOHPDWPLVERAULVSYKLAVGR-SYEPOLCPYLGHVSUSGLNVLDLDRABELHVK 291

RESULT 3

Db 292 VKTLEEBADYLGQVKIGERVTLWMOIGETWDPSKREILKYLDRDVSTMGLAKEFLP 351  
 Qy 368 FAIQLSVTGFLPDQGAMSFGPRFLWLRBAFKELPNRVERPPEETRGATVLEPL 427  
 Db 352 FGBELSVGSPGLDQTMASVGPFLRWRLEERAKUGLVEVNRVENSEGRAGATVLPK 411

Qy 428 RGVHENIAVUDPSMWPNIKINVGDPDTLVRGEKCGECGCWEAPEVKHRFRCCPGF 487  
 Db 412 PGHEDIAVFLPASWKPNIKMYKNGDPDTLVRGEYGESEVYTAPEGHCFPKSPGPFP 471

Qy 548 CKAVTAWGRHLRTANIARKLGLKLVYGDPSLTVTYDPKVENFIKIKKEELGFEIK 607  
 Db 532 CABAVTAWGRHLRTANIARKLGLKLVYGDPSLTVTYDPKVENFIKIKKEELGFEIK 591

Qy 608 LSKYKVLFLPEAKKRYAGLJEDGRIDIVGFEEVRGDWCELAKEVQKA 667  
 Db 592 VDKVYRVEFPEAKRGRVGLTVDGKIDVGFEEVRGDWCELAKEVQKA 651

Qy 668 KAVEYVRKIVKELBEKGKPVIEKVIKTSLKRUVEYTYDQDIIPALRLIGY 727  
 Db 652 EAVDYVNRNIEKLRQQDVKLVIKNTLTPPSMVEARQHVTALLMEBAGIKYEGA 711

Qy 728 KIGYVYVKGGERISORAMPYFMKPSOIDTYDQDIIPALRLIGYFCTEKKUKAS 787  
 Db 712 KIGYVYVKGSGLYTRAKYPTMA-SKEBEDFYYVQVPAFLRLIQYFCTEKKUKAS 770

Qy 788 ATGQKTLDFLACK 800  
 Db 771 GR-QSTLDFMR 782

Qy 728 KIGYVYVKGGERISORAMPYFMKPSOIDTYDQDIIPALRLIGYFCTEKKUKAS 787  
 C;Species: Sulfurisphaera ohwakuenensis C;Accession: JC7382 C;Date: 17-Nov-2000 #Sequence\_revision 17-Nov-2000 #text\_change 31-Dec-2000 C;Comment: This enzyme has both 3'-5' exonuclease and polymerase activities, and play a role in DNA replication, exconuclease, metal binding, nucleotidyltransferase, C;Keywords: DNA replication; exonuclease; metal binding; nucleotidyltransferase A;Gene: B3 A;Molecule type: DNA A;Residues: 1-781 <RAW> A;Cross-references: DDBJ:AB032376 C;Comment: This enzyme has both 3'-5' exonuclease and polymerase activities, and play a role in DNA replication, exconuclease, metal binding, nucleotidyltransferase

Query Match 53.6%; Score 2246; DB 2; Length 781; Best Local Similarity 54.3%; Pred. No. 9.9e-129; Matches 432; Conservative 141; Mismatches 203; Indels 20; Gaps 10;

Qy 6 FPTLDSYEVGKEPQVITWGAEMGRVWLDSPRYPVALLPGADPKQVQAIRAL 65  
 Db 5 FFILDESDYDVENPKVYIWIKEDEKGRVWILKKEFPRPYFVALVDDSYNIDEIRKEILK 64

Qy 66 SRPKSPSPIGEVKRKYGRRRVIRTVLPEAREYRELYVNDGVEDVLEADIRFAM 125  
 Db 65 SKVSPSITSBVEKKYFGSPVVKLIEFVPIAVYRVRDVEVAKTIGKVSFLRADIFYM 124

Qy 126 RYLDIDLPPFTWYRVEAEPLENKQAFPRDKVYLVKVSRPEPLYGEALAPTKLDRILAF 185  
 Db 125 RYSDINLKPFWIEVEEKEN-NFREVKEK-KINKLEYED----KIPBLKVLAF 177

Qy 186 DIVEYSKGSRPRPERPVIVIAVKTDDGDSVFLIAEGKDDKPKIREPVEVYKVPDII 245

## BEST AVAILABLE COR

QY 421 AIVVERPLRGHENIAVLDSSMSYPMIMKINGPDTLVARGBKCGCGWBAPIVHFR 480  
 Db 421 AIVVERPLRGHENIAVLDSSMSYPMIMKINGPDTLVARGBKCGCGWBAPIVHFR 480  
 QY 481 RCPPGPKTIVLRLERLRLRKRVRRAEMKKYPPDSPEPDRPLDPRKALKVLANASYGMNSQ 540  
 Db 481 RCPPGPKTIVLRLERLRLRKRVRRAEMKKYPPDSPEPDRPLDPRKALKVLANASYGMNSQ 540  
 QY 541 ARWYCRCAKAVTAGWGRHLIRTAINTARKUGLKUYGDPDSFLVTPYDPEKVENTIKE 600  
 Db 541 ARWYCRCAKAVTAGWGRHLIRTAINTARKUGLKUYGDPDSFLVTPYDPEKVENTIKE 600  
 QY 601 ELGFRIKLEKVKYKLFPTEAKRKYAGLLEDGRIDIVGFEAVRGDCELAKEVOTRVETV 660  
 Db 601 ELGFRIKLEKVKYKLFPTEAKRKYAGLLEDGRIDIVGFEAVRGDCELAKEVOTRVETV 660  
 QY 661 LKTSVSENVKAYEVRKIVKVLBEGKVPIEKVLUWTKSRLREYTTAEPVAAKEMLSAG 720  
 Db 661 LKTSVSENVKAYEVRKIVKVLBEGKVPIEKVLUWTKSRLREYTTAEPVAAKEMLSAG 720  
 QY 721 YRVSPDKIGVYVKGGRISORAWPYFMVWQPSQDVTYVWDHQIIPALRILGYFGIT 780  
 Db 721 YRVSPDKIGVYVKGGRISORAWPYFMVWQPSQDVTYVWDHQIIPALRILGYFGIT 780  
 QY 781 EKUKASATGQTLPLAKSK 803  
 Db 781 EKUKASATGQTLPLAKSK 803

**RESULT 2**

US-08-062-368-4  
 Sequence 4, Application US/08062368  
 ; Patent No. 5491086  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gelfand, David H.  
 ; ADDRESS: Hoffmann-La Roche Inc.  
 ; STREET: 340 Kingsland Street  
 ; CITY: Nutley  
 ; STATE: New Jersey  
 ; COUNTRY: U.S.A.  
 ; ZIP: 07110

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/062,368  
 FILING DATE: 1993/5/14  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: S. ab Ph.D., Stacey R.  
 REGISTRATION NUMBER: 32,630  
 REFERENCE/DOCKET NUMBER: 8584  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (510) 814-2863  
 TELEX/FAX: (510) 814-2977  
 INFORMATION FOR SEQ ID NO: 4:  
 SOURCE/CHARACTERISTICS:  
 LENGTH: 803 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 QY 72.3%; Score 3028.5; DB 1; Length 803;

**Best Local Similarity 70.8%; Pred. No. 1e-270; Matches 570; Conservative 106; Mismatches 122; Indels 7; Gaps 5;**  
**Db 1 MTEVV-FTVLSSSYEVGKRPQVINGIAENGERVVLIDSFRPYFTTALLPGADP--KO 57.**  
**Db 1 MTEVV-FTVLSSSYEVGKRPQVINGIAENGERVVLIDSFRPYFTTALLPGADP--KO 57.**  
**Qy 58 VADQRIRALSRPKSPICGVEDDRKRYGPRPRVDRIRVLPVBRVREBLVNDGDEV 117**  
**Db 61 IASIRRLSVVKSPIADKPLDKYFGRPRCKVKTWIPESVRHREAVKLEGEDSL 120**  
**Qy 118 EADTRPAMYLLDHDLPPTWTRVLEAPLENOMGFRUDKVLYKSREPPLGEALAPTKL 177**  
**Db 121 EADTRPAMYLLDHDLPPTWTRVLEAPLENOMGFRUDKVLYKSREPPLGEALAPTKL 177**  
**Db 178 PDLRILAFDIEVNSVSKQSPRPRDPVVIANKTDDGDEVFLTAGKDODRKPREFEVK 237**  
**Db 179 PPRLVLADEVSRSRSPNPARDPVVLSRDRSSEGKRLIEAGHODRVRUREFVEV 238**  
**Qy 238 YVDIDTGYNNHNPWDYVLLRKAARTGKIDVTRVGAEPSTSVRHVSVERLANDLY 297**  
**Db 239 AFPDIDTGYNSHFDWYLMERARRUGINLDVTRVGAEPSTSVRHVSVERLANDLY 298**  
**Qy 298 DYBREMPPEKIKSLEEVEAVALGMMKKSERVITINWEVDYMDPDKPKEPLQYARDVRA 357**  
**Db 299 DYAZEMPEKIKTLEBEVARYLGMMKKSERVITINWEVDYMDPDKPKEPLQYARDVRA 358**  
**Qy 358 TYSLAEKULPFAQLSYTGVLQDVGAMSVERLEMLIRAKMCELVPERVERBET 417**  
**Db 359 TYGLAEKULPFAQLSTVGTGPVLDQVGAMGVRFLWYMLRDAYMNEBLUPNVERGES 418**  
**Qy 418 YRGAVLVERPLRGHENIAVLDSSMSYPMIMKINGPDTLVARGBKCGCGWBAPIVHFR 476**  
**Db 419 YKGAIVVRLPLKGHENVVVLDFSSMSYPMIMKINGPDTLVARGBKCGCGWBAPIVHFR 478**  
**Qy 477 HRFRCPGPKTIVLRLERLRLRKRVRRAEMKKYPPDSPEPDRPLDPRKALKVLANASYM 536**  
**Db 479 HRFRCPGPKTIVLRLERLRLRKRVRRAEMKKYPPDSPEPDRPLDPRKALKVLANASYM 538**  
**Qy 537 GWSGARWTCRECAKAVTAGWGRHLIRTAINTARKUGLKUYGDPDSFLVTPYDPEKVENFIK 596**  
**Db 539 GWSHARWYCRCAKAVTAGWGRHLIRTAINTARKUGLKUYGDPDSFLVTPYDPEKVENFIK 598**  
**Qy 597 LIKELGFIKLEKVKYKLFPTEAKRKYAGLLEDGRIDIVGFEAVRGDCELAKEVOKV 656**  
**Db 599 FVEKLGEPKIKOIKYKUFTTEAKRKYAGLLEDGRIDIVGFEAVRGDCELAKEVOKV 658**  
**Qy 657 VETVLTSENVKAYEVRKIVKVLBEGKVPIEKVLUWTKSRLREYTTAEPVAAKEM 716**  
**Db 659 AEVLTNGDVKAISSYEVKQJLREGKVPIEGLWTKSRLREYTTAEPVAAKEM 718**  
**Qy 717 LSGYRVSPDKIGVYVKGGRISORAWPYFMVWQPSQDVTYVWDHQIIPALRILGY 776**  
**Db 719 KEAGYEVSPGDKGKVYVWVKGSGSVSRAVYPFW-DPSRIDWVYIDHQIIPALRILSY 777**  
**Qy 777 FGTTERKLSATCORTDFPLACK 801**  
**Db 778 FGVIEKQLKAAATVQRLSDFFPLASK 802**

**RESULT 3**

US-08-062-368-2  
 Sequence 2, Application US/08062368  
 ; Patent No. 5491086  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gelfand, David H.  
 ; ADDRESS: Hoffmann-La Roche Inc.  
 ; STREET: 340 Kingsland Street